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* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1            Web Page for STN Seminar Schedule - N. America
 NEWS  2  NOV 21    CAS patent coverage to include exemplified prophetic
                    substances identified in English-, French-, German-,
                    and Japanese-language basic patents from 2004-present
 NEWS  3  NOV 26    MARPAT enhanced with FSORT command
 NEWS  4  NOV 26    CHEMSAFE now available on STN Easy
 NEWS  5  NOV 26    Two new SET commands increase convenience of STN
                    searching
 NEWS  6  DEC 01    ChemPort single article sales feature unavailable
 NEWS  7  DEC 12    GBFULL now offers single source for full-text
                    coverage of complete UK patent families
 NEWS  8  DEC 17    Fifty-one pharmaceutical ingredients added to PS
 NEWS  9  JAN 06    The retention policy for unread STNmail messages
                    will change in 2009 for STN-Columbus and STN-Tokyo
 NEWS 10  JAN 07    WPIDS, WPINDEX, and WPIX enhanced Japanese Patent
                    Classification Data
 NEWS 11  FEB 02    Simultaneous left and right truncation (SLART) added
                    for CERAB, COMPUAB, ELCOM, and SOLIDSTATE
 NEWS 12  FEB 02    GENBANK enhanced with SET PLURALS and SET SPELLING
 NEWS 13  FEB 06    Patent sequence location (PSL) data added to USGENE
 NEWS 14  FEB 10    COMPENDEX reloaded and enhanced
 NEWS 15  FEB 11    WTEXTILES reloaded and enhanced

 NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
              AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

 NEWS HOURS     STN Operating Hours Plus Help Desk Availability
 NEWS LOGIN     Welcome Banner and News Items
 NEWS IPC8      For general information regarding STN implementation of IPC 8

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FILE 'HOME' ENTERED AT 12:49:44 ON 12 FEB 2009

=> caplus
THIS COMMAND NOT AVAILABLE IN THE CURRENT FILE
Some commands only work in certain files.  For example, the EXPAND
command can only be used to look at the index in a file which has an
index.  Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of
commands which can be used in this file.

=> file caplus
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.22       0.22

FILE 'CAPLUS' ENTERED AT 12:50:23 ON 12 FEB 2009
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FILE COVERS 1907 - 12 Feb 2009 VOL 150 ISS 7
FILE LAST UPDATED: 11 Feb 2009 (20090211/ED)

Caplus now includes complete International Patent Classification (IPC)
reclassification data for the third quarter of 2008.

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This file contains CAS Registry Numbers for easy and accurate
substance identification.

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=> antibody
        342815 ANTIBODY
        413274 ANTIBODIES
L1      546015 ANTIBODY
                  (ANTIBODY OR ANTIBODIES)

=> monoclonal
        159505 MONOCLONAL
           560 MONOCLONALS
L2      159578 MONOCLONAL
                  (MONOCLONAL OR MONOCLONALS)

=> single chain
       1483267 SINGLE
          3557 SINGLES
       1486279 SINGLE
                  (SINGLE OR SINGLES)
        802222 CHAIN
        342735 CHAINS
       1004346 CHAIN
                  (CHAIN OR CHAINS)
L3       15140 SINGLE CHAIN
                  (SINGLE(W)CHAIN)

=> fragment
        222617 FRAGMENT
        215174 FRAGMENTS
L4      381669 FRAGMENT
                  (FRAGMENT OR FRAGMENTS)

=> coronivirus
L5            0 CORONIVIRUS

=> coronavirus
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          5817 CORONAVIRUS
          1038 CORONAVIRUSES
L6        5940 CORONAVIRUS
                 (CORONAVIRUS OR CORONAVIRUSES)

=> SARS
L7        4917 SARS

=> L1 and L2
L8      155125 L1 AND L2

=> L1
        342815 ANTIBODY
        413274 ANTIBODIES
L9      546015 ANTIBODY
                 (ANTIBODY OR ANTIBODIES)

=> L6 and L1
L10       1537 L6 AND L1

=> L2 and L10
L11        495 L2 AND L10

=> L7 and L1
L12       1026 L7 AND L1

=> L12 and L2
L13        238 L12 AND L2

=> nucleoprotein
          8472 NUCLEOPROTEIN
          6679 NUCLEOPROTEINS
L14      11936 NUCLEOPROTEIN
                 (NUCLEOPROTEIN OR NUCLEOPROTEINS)

=> L14 and L11
L15         15 L14 AND L11

=> L14 and L13
L16          8 L14 AND L13

=> L5 and L14
L17          0 L5 AND L14

=> L6 and L14
L18         98 L6 AND L14

=> L7 and L14
L19         47 L7 AND L14

=> L2 and L18
L20         16 L2 AND L18

=> L2 and L19
L21          8 L2 AND L19

=> D L21 IBIB ABS 1-8

L21  ANSWER 1 OF 8  CAPLUS  COPYRIGHT 2009 ACS on STN
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Full Text | Citing References

ACCESSION NUMBER: 2007:147094 CAPLUS
DOCUMENT NUMBER: 147:46687
TITLE: Cloning, expressing and antigenicity analysis of nucleocapsid proteins of SARS-CoV, HCoV-229E and OC43
AUTHOR(S): Che, Xiaoyan; Liao, Zhiyong; Wang, Yadi; Qiu, Liwen; Wen, Kun; Pan, Yuxian; Xu, Hua; Mei, Yabo; Hao, Wei; Ding, Yanqing
CORPORATE SOURCE: Zhujiang Hospital, Southern Medical University, Guangzhou, 510282, Peop. Rep. China
SOURCE: Zhonghua Weishengwuxue He Mianyixue Zazhi (2005), 25(9), 711-715
CODEN: ZWMZDP; ISSN: 0254-5101
PUBLISHER: Beijing Shengwu Zhipin Yanjiuso
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB A recombinant nucleocapsid (N) protein of SARS-CoV, HCoV-229E and HCoV-OC43, was obtained resp. to study antigenic relationships of N proteins between SARS-CoV and human coronaviruses 229E and OC43. The genes encoding the full-length of N proteins from SARS-CoV, HCoV-229E and HCoV-OC43 were amplified by RT-PCR and cloned into the prokaryotic expression vector pQE30. The His6-tagged N proteins were expressed in the M15 strain and further purified with affinity chromatog. The antigenicity of N proteins was analyzed by Western blot and immunofluorescence assay. The N genes of 1281, 1182 and 1359 bp from SARS-CoV, HCoV-229E and HCoV-OC43, resp. were amplified with their corresponding primer pairs. The recombinant plasmids were sequenced, and they were all in frame with sequences matching those for the N genes of the three coronaviruses. The expressed recombinant His6-tagged N proteins were identified by Western blot assay with anti-His tag monoclonal antibody. The immunoreactive protein bands with expected sizes were 47 kDa, 44 kDa and 50 kDa from SARS-CoV, HCoV-229E and HCoV-OC43, resp. The nucleocapsid proteins of SARS-CoV, HCoV-229E and HCoV-OC43 strongly and specifically reacted with the virus specific rabbit serum and with the nucleoprotein specific murine serum. No cross-reactivity was found among the nucleocapsid proteins of SARS-CoV, HCoV-229E and HCoV-OC43. The immunogenic nucleocapsid recombinant proteins from SARS-CoV, HCoV-229E and HCoV-OC43 were obtained. There was no antigenic relationship among the three N proteins.

L21 ANSWER 2 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | RefQ References

ACCESSION NUMBER: 2006:1263772 CAPLUS
DOCUMENT NUMBER: 146:137159
TITLE: Coronavirus nucleocapsid protein is an RNA chaperone
AUTHOR(S): Zuniga, Sonia; Sola, Isabel; Moreno, Jose L.; Sabella, Patricia; Plana-Duran, Juan; Enjuanes, Luis
CORPORATE SOURCE: Centro Nacional de Biotecnologia, CSIC, Department of Molecular and Cell Biology, Campus Universidad Autonoma, Madrid, 28049, Spain
SOURCE: Virology (2007), 357(2), 215-227
CODEN: VIRLAX; ISSN: 0042-6822
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB RNA chaperones are nonspecific nucleic acid binding proteins with long disordered regions that help RNA mols. to adopt its functional conformation. Coronavirus nucleoproteins (N) are nonspecific

RNA-binding proteins with long disordered regions. Therefore, we investigated whether transmissible gastroenteritis coronavirus (TGEV) N protein was an RNA chaperone. Purified N protein enhanced hammerhead ribozyme self-cleavage and nucleic acids annealing, which are properties that define RNA chaperones. In contrast, another RNA-binding protein, PTB, did not show these activities. N protein chaperone activity was blocked by specific monoclonal antibodies. Therefore, it was concluded that TGEV N protein is an RNA chaperone. In addn., we have shown that purified severe acute respiratory syndrome (SARS)-CoV N protein also has RNA chaperone activity. In silico predictions of disordered domains showed a similar pattern for all coronavirus N proteins evaluated. Altogether, these data led us to suggest that all coronavirus N proteins might be RNA chaperones.

REFERENCE COUNT: 83 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | More References

ACCESSION NUMBER: 2006:1139612 CAPLUS
DOCUMENT NUMBER: 146:140843
TITLE: Antigenic and cellular localisation analysis of the severe acute respiratory syndrome coronavirus nucleocapsid protein using monoclonal antibodies
AUTHOR(S): Bussmann, Bianca M.; Reiche, Sven; Jacob, Lotta H.; Braun, Jan Matthias; Jassoy, Christian
CORPORATE SOURCE: Institute of Virology, University of Leipzig, Leipzig, 04103, Germany
SOURCE: Virus Research (2006), 122(1-2), 119-126
CODEN: VIREDF; ISSN: 0168-1702
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A member of the family of coronaviruses has previously been identified as the cause of the severe acute respiratory syndrome (SARS). In this study, several monoclonal antibodies against the nucleocapsid protein have been generated to examine distribution of the nucleocapsid in virus-infected cells and to study antigenic regions of the protein. Confocal microscopic anal. identified nucleocapsids packaged in vesicles in the perinuclear area indicating viral synthesis at the endoplasmic reticulum and Golgi app. The monoclonal antibodies bound to the central and carboxyterminal half of the nucleocapsid protein indicating prominent exposure and immunogenicity of this part of the protein. Antibodies recognized both linear and conformational epitopes. Predictions of antigenicity using amt.. modeling based on hydrophobicity anal. of SARS nucleoprotein could not be confirmed fully. Antibody binding to discontinuous peptides provides evidence that amino acids 274-283 and 373-382 assemble to a structural unit particularly rich in basic amino acids. In addn., amino acids 286-295, 316-325 and 361-367 that represent the epitope recognized by monoclonal antibody 6D11C1 converge indicating a well-structured C-terminal region of the SARS virus nucleocapsid protein and functional relation of the peptide regions involved. Alternatively, dimerization of the nucleocapsid protein may result in juxtaposition of the amino acid sequences 316-325 and 361-367 on one nucleoprotein mol. to amino acid 286-295 on the second peptide. The monoclonal antibodies will be available to assess antigenicity and immunol. variabilities between different SARS CoV strains.

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2006:236188 CAPLUS
DOCUMENT NUMBER: 145:185561
TITLE: Time course and cellular localization of SARS-CoV nucleoprotein and RNA in lungs from fatal cases of SARS
AUTHOR(S): Nicholls, John M.; Butany, Jagdish; Poon, Leo L. M.; Chan, Kwok H.; Beh, Swan Lip; Poutanen, Susan; Peiris, J. S. Malik; Wong, Maria
CORPORATE SOURCE: Department of Pathology, The University of Hong Kong, Pok Fu Lam, Hong Kong SAR, Peop. Rep. China
SOURCE: PLoS Medicine (2006), 3(2), 222-229
CODEN: PMLEAC; ISSN: 1549-1277
URL: http://medicine.plosjournals.org/archive/1549-1676/3/2/pdf/10.1371_1549-1676_3_2_complete.pdf
PUBLISHER: Public Library of Science
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English

AB Background: Cellular localization of severe acute respiratory syndrome coronavirus (SARS-CoV) in the lungs of patients with SARS is important in confirming the etiol. assocn. of the virus with disease as well as in understanding the pathogenesis of the disease. To our knowledge, there have been no comprehensive studies investigating viral infection at the cellular level in humans. Methods and Findings: We collected the largest series of fatal cases of SARS with autopsy material to date by merging the pathol. material from two regions involved in the 2003 worldwide SARS outbreak in Hong Kong, China, and Toronto, Canada. We developed a monoclonal antibody against the SARS-CoV nucleoprotein and used it together with in situ hybridization (ISH) to analyze the autopsy lung tissues of 32 patients with SARS from Hong Kong and Toronto. We compared the results of these assays with the pulmonary pathologies and the clin. course of illness for each patient. SARS-CoV nucleoprotein and RNA were detected by immunohistochem. and ISH, resp., primarily in alveolar pneumocytes and, less frequently, in macrophages. Such localization was detected in four of the seven patients who died within two weeks of illness onset, and in none of the 25 patients who died later than two weeks after symptom onset. Conclusions: The pulmonary alveolar epithelium is the chief target of SARS-CoV, with macrophages infected subsequently. Viral replication appears to be limited to the first two weeks after symptom onset, with little evidence of continued widespread replication after this period. If antiviral therapy is considered for future treatment, it should be focused on this two-week period of acute clin. disease.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2005:409560 CAPLUS
DOCUMENT NUMBER: 142:462283
TITLE: Monoclonal antibodies specific to SARS virus nucleoprotein for immunodiagnosis of SARS
INVENTOR(S): Uchida, Yoshiaki; Fujii, Nobuyuki; Kurano, Yoshihiro; Okada, Masahisa; Kogaki, Hiroyuki; Kido, Yasuji; Miyake, Kazushige
PATENT ASSIGNEE(S): Fujirebio Inc., Japan
SOURCE: PCT Int. Appl., 41 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005042579	A1	20050512	WO 2004-JP16099	20041029
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CN 1902230	A	20070124	CN 2004-80039648	20041029
IN 2006KN01457	A	20070504	IN 2006-KN1457	20060530
US 20080254440	A1	20081016	US 2007-577310	20070222
PRIORITY APPLN. INFO.:			JP 2003-373779 A	20031031
			JP 2004-34268 A	20040210
			WO 2004-JP16099 W	20041029

AB Provided are monoclonal antibodies specific to SARS virus nucleoprotein and hybridomas producing them. These monoclonal antibodies are labeled with enzyme and used for immunodiagnosis of SARS.
REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN
Full Text | Citing References

ACCESSION NUMBER: 2004:872877 CAPLUS
DOCUMENT NUMBER: 141:378847
TITLE: Endogenous host elements or viral-based sequence elements for diagnosis, prognosis and therapy of viral infection, autoimmune disease and lymphoproliferative disease
INVENTOR(S): Hu, Yu-wen; Brown, Earl
PATENT ASSIGNEE(S): Canadian Blood Services, Can.
SOURCE: PCT Int. Appl., 174 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004090544	A2	20041021	WO 2004-CA544	20040413
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ,				

BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

CA 2522067	A1	20041021	CA 2004-2522067	20040413
EP 1625402	A2	20060215	EP 2004-726942	20040413
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR				
US 20060115875	A1	20060601	US 2005-248008	20051011
PRIORITY APPLN. INFO.:			US 2003-461137P	P 20030409
			US 2003-506779P	P 20030930
			WO 2004-CA544	W 20040413

AB A method of detecting, characterizing and treating viral infection, autoimmune disease and lymphoproliferative disease is provided. In particular, a strategy of mol. mimicry is provided for characterizing viral behavior and/or a predisposition for a given viral outcome in vivo. Novel compns. are also provided for detecting, characterizing and treating viral infections. The viral infection is caused by HCV, HIV, HTLV-1, HTLV-2, SARS-CoV, or a member of Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae, Poxviridae or Coronaviridae. The viral-based sequence element is e.g. an element of S protein sequence of an ORF1a protein sequence of SARS-CoV; a Gag, Pol or Env polyprotein of HTLV-1; a NS5A and E2 protein of HCV; bacterial virulence factor; human endogenous retrovirus element; Peyer's patches virulence factor gipA; or an Ig selected from IgG, IgA, IgM, IgD or IgE. The treatment regime includes an anti-viral monoclonal or polyclonal antibody, or a compd. capable of binding epitope of the endogenous host element.

L21 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | RN Q References

ACCESSION NUMBER:	2004:541777 CAPLUS
DOCUMENT NUMBER:	141:222968
TITLE:	Organ distribution of severe acute respiratory syndrome (SARS) associated coronavirus (SARS-CoV) in SARS patients: implications for pathogenesis and virus transmission pathways
AUTHOR(S):	Ding, Yanqing; He, Li; Zhang, Qingling; Huang, Zhongxi; Che, Xiaoyan; Hou, Jinlin; Wang, Huijun; Shen, Hong; Qiu, Liwen; Li, Zhuguo; Geng, Jian; Cai, Junjie; Han, Huixia; Li, Xin; Kang, Wei; Weng, Desheng; Liang, Ping; Jiang, Shibo
CORPORATE SOURCE:	Department of Pathology, Nan Fang Hospital, First Military Medical University, Guangzhou, Peop. Rep. China
SOURCE:	Journal of Pathology (2004), 203(2), 622-630 CODEN: JPTLAS; ISSN: 0022-3417
PUBLISHER:	John Wiley & Sons Ltd.
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB We previously identified the major pathol. changes in the respiratory and immune systems of patients who died of severe acute respiratory syndrome (SARS) but gained little information on the organ distribution of SARS-assocd. coronavirus (SARS-CoV). In the present study, we used a murine monoclonal antibody specific for SARS-CoV nucleoprotein, and probes specific for a SARS-CoV RNA polymerase gene fragment, for immunohistochem. and in situ hybridization, resp., to detect SARS-CoV systematically in tissues from patients who died of SARS. SARS-CoV was found in lung, trachea/bronchus, stomach, small intestine, distal convoluted renal tubule, sweat gland, parathyroid, pituitary, pancreas,

adrenal gland, liver and cerebrum, but was not detected in esophagus, spleen, lymph node, bone marrow, heart, aorta, cerebellum, thyroid, testis, ovary, uterus or muscle. These results suggest that, in addn. to the respiratory system, the gastrointestinal tract and other organs with detectable SARS-CoV may also be targets of SARS-CoV infection. The pathol. changes in these organs may be caused directly by the cytopathic effect mediated by local replication of the SARS-CoV; or indirectly as a result of systemic responses to respiratory failure or the harmful immune response induced by viral infection. In addn. to viral spread through a respiratory route, SARS-CoV in the intestinal tract, kidney and sweat glands may be excreted via feces, urine and sweat, thereby leading to virus transmission. This study provides important information for understanding the pathogenesis of SARS-CoV infection and sheds light on possible virus transmission pathways. This data will be useful for designing new strategies for prevention and treatment of SARS.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2004:539287 CAPLUS
DOCUMENT NUMBER: 141:275951
TITLE: Development and characterisation of neutralising monoclonal antibody to the SARS-coronavirus
AUTHOR(S): Berry, Jody D.; Jones, Steven; Drebot, Michael A.; Andonov, Anton; Sabara, Marta; Yuan, Xin Y.; Weingartl, Hana; Fernando, Lisa; Marszal, Peter; Gren, Jason; Nicolas, Brigitte; Andonova, Maya; Ranada, Francesca; Gubbins, Michael J.; Ball, T. Blake; Kitching, Paul; Li, Yan; Kabani, Amin; Plummer, Frank
CORPORATE SOURCE: Department of Medical Microbiology, National Centre for Foreign Animal Disease, CFIA, University of Manitoba, Winnipeg, Can.
SOURCE: Journal of Virological Methods (2004), 120(1), 87-96 CODEN: JVMEDH; ISSN: 0166-0934
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB There is a global need to elucidate protective antigens expressed by the SARS-coronavirus (SARS-CoV). Monoclonal antibody reagents that recognize specific antigens on SARS-CoV are needed urgently. In this report, the development and immunochem. characterization of a panel of murine monoclonal antibodies (mAbs) against the SARS-CoV is presented, based upon their specificity, binding requirements, and biol. activity. Initial screening by ELISA, using highly purified virus as the coating antigen, resulted in the selection of 103 mAbs to the SARS virus. Subsequent screening steps reduced this panel to seventeen IgG mAbs. A single mAb, F26G15, is specific for the nucleoprotein as seen in Western immunoblot while five other mAbs react with the Spike protein. Two of these Spike-specific mAbs demonstrate the ability to neutralize SARS-CoV in vitro while another four Western immunoblot-neg. mAbs also neutralize the virus. The utility of these mAbs for diagnostic development is demonstrated. Antibody from convalescent SARS patients, but not normal human serum, is also shown to specifically compete off binding of mAbs to whole SARS-CoV. These studies highlight the importance of using standardized assays and reagents. These mAbs will be useful for the development of diagnostic tests, studies of SARS-CoV pathogenesis and vaccine development.

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> D L20 IBIB ABS 1-16

L20 ANSWER 1 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Chng Reference

ACCESSION NUMBER: 2007:147094 CAPLUS
DOCUMENT NUMBER: 147:46687
TITLE: Cloning, expressing and antigenicity analysis of nucleocapsid proteins of SARS-CoV, HCoV-229E and OC43
AUTHOR(S): Che, Xiaoyan; Liao, Zhiyong; Wang, Yadi; Qiu, Liwen; Wen, Kun; Pan, Yuxian; Xu, Hua; Mei, Yabo; Hao, Wei; Ding, Yanqing
CORPORATE SOURCE: Zhujiang Hospital, Southern Medical University, Guangzhou, 510282, Peop. Rep. China
SOURCE: Zhonghua Weishengwuxue He Mianyixue Zazhi (2005), 25(9), 711-715
CODEN: ZWMZDP; ISSN: 0254-5101
PUBLISHER: Beijing Shengwu Zhipin Yanjiuso
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB A recombinant nucleocapsid (N) protein of SARS-CoV, HCoV-229E and HCoV-OC43, was obtained resp. to study antigenic relationships of N proteins between SARS-CoV and human coronaviruses 229E and OC43. The genes encoding the full-length of N proteins from SARS-CoV, HCoV-229E and HCoV-OC43 were amplified by RT-PCR and cloned into the prokaryotic expression vector pQE30. The His6-tagged N proteins were expressed in the M15 strain and further purified with affinity chromatog. The antigenicity of N proteins was analyzed by Western blot and immunofluorescence assay. The N genes of 1281, 1182 and 1359 bp from SARS-CoV, HCoV-229E and HCoV-OC43, resp. were amplified with their corresponding primer pairs. The recombinant plasmids were sequenced, and they were all in frame with sequences matching those for the N genes of the three coronaviruses. The expressed recombinant His6-tagged N proteins were identified by Western blot assay with anti-His tag monoclonal antibody. The immunoreactive protein bands with expected sizes were 47 kDa, 44 kDa and 50 kDa from SARS-CoV, HCoV-229E and HCoV-OC43, resp. The nucleocapsid proteins of SARS-CoV, HCoV-229E and HCoV-OC43 strongly and specifically reacted with the virus specific rabbit serum and with the nucleoprotein specific murine serum. No cross-reactivity was found among the nucleocapsid proteins of SARS-CoV, HCoV-229E and HCoV-OC43. The immunogenic nucleocapsid recombinant proteins from SARS-CoV, HCoV-229E and HCoV-OC43 were obtained. There was no antigenic relationship among the three N proteins.

L20 ANSWER 2 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Chng Reference

ACCESSION NUMBER: 2006:1263772 CAPLUS
DOCUMENT NUMBER: 146:137159
TITLE: Coronavirus nucleocapsid protein is an RNA chaperone
AUTHOR(S): Zuniga, Sonia; Sola, Isabel; Moreno, Jose L.; Sabella, Patricia; Plana-Duran, Juan; Enjuanes, Luis
CORPORATE SOURCE: Centro Nacional de Biotecnologia, CSIC, Department of Molecular and Cell Biology, Campus Universidad Autonoma, Madrid, 28049, Spain
SOURCE: Virology (2007), 357(2), 215-227
CODEN: VIRLAX; ISSN: 0042-6822

PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB RNA chaperones are nonspecific nucleic acid binding proteins with long disordered regions that help RNA mols. to adopt its functional conformation. Coronavirus nucleoproteins (N) are nonspecific RNA-binding proteins with long disordered regions. Therefore, we investigated whether transmissible gastroenteritis coronavirus (TGEV) N protein was an RNA chaperone. Purified N protein enhanced hammerhead ribozyme self-cleavage and nucleic acids annealing, which are properties that define RNA chaperones. In contrast, another RNA-binding protein, PTB, did not show these activities. N protein chaperone activity was blocked by specific monoclonal antibodies. Therefore, it was concluded that TGEV N protein is an RNA chaperone. In addn., we have shown that purified severe acute respiratory syndrome (SARS)-CoV N protein also has RNA chaperone activity. In silico predictions of disordered domains showed a similar pattern for all coronavirus N proteins evaluated. Altogether, these data led us to suggest that all coronavirus N proteins might be RNA chaperones.
REFERENCE COUNT: 83 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 3 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2006:1139612 CAPLUS
DOCUMENT NUMBER: 146:140843
TITLE: Antigenic and cellular localisation analysis of the severe acute respiratory syndrome coronavirus nucleocapsid protein using monoclonal antibodies
AUTHOR(S): Bussmann, Bianca M.; Reiche, Sven; Jacob, Lotta H.; Braun, Jan Matthias; Jassoy, Christian
CORPORATE SOURCE: Institute of Virology, University of Leipzig, Leipzig, 04103, Germany
SOURCE: Virus Research (2006), 122(1-2), 119-126
CODEN: VIREDF; ISSN: 0168-1702
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A member of the family of coronaviruses has previously been identified as the cause of the severe acute respiratory syndrome (SARS). In this study, several monoclonal antibodies against the nucleocapsid protein have been generated to examine distribution of the nucleocapsid in virus-infected cells and to study antigenic regions of the protein. Confocal microscopic anal. identified nucleocapsids packaged in vesicles in the perinuclear area indicating viral synthesis at the endoplasmic reticulum and Golgi app. The monoclonal antibodies bound to the central and carboxyterminal half of the nucleocapsid protein indicating prominent exposure and immunogenicity of this part of the protein. Antibodies recognized both linear and conformational epitopes. Predictions of antigenicity using amt.. modeling based on hydrophobicity anal. of SARS nucleoprotein could not be confirmed fully. Antibody binding to discontinuous peptides provides evidence that amino acids 274-283 and 373-382 assemble to a structural unit particularly rich in basic amino acids. In addn., amino acids 286-295, 316-325 and 361-367 that represent the epitope recognized by monoclonal antibody 6D11C1 converge indicating a well-structured C-terminal region of the SARS virus nucleocapsid protein and functional relation of the peptide regions involved. Alternatively, dimerization of the nucleocapsid protein may result in juxtaposition of the amino acid sequences 316-325 and 361-367 on one nucleoprotein mol.

to amino acid 286-295 on the second peptide. The monoclonal antibodies will be available to assess antigenicity and immunol. variabilities between different SARS CoV strains.

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 4 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Cited References

ACCESSION NUMBER: 2006:236188 CAPLUS
DOCUMENT NUMBER: 145:185561
TITLE: Time course and cellular localization of SARS-CoV nucleoprotein and RNA in lungs from fatal cases of SARS
AUTHOR(S): Nicholls, John M.; Butany, Jagdish; Poon, Leo L. M.; Chan, Kwok H.; Beh, Swan Lip; Poutanen, Susan; Peiris, J. S. Malik; Wong, Maria
CORPORATE SOURCE: Department of Pathology, The University of Hong Kong, Pok Fu Lam, Hong Kong SAR, Peop. Rep. China
SOURCE: PLoS Medicine (2006), 3(2), 222-229
CODEN: PMLEAC; ISSN: 1549-1277
URL: http://medicine.plosjournals.org/archive/1549-1676/3/2/pdf/10.1371_1549-1676_3_2_complete.pdf
PUBLISHER: Public Library of Science
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English

AB Background: Cellular localization of severe acute respiratory syndrome coronavirus (SARS-CoV) in the lungs of patients with SARS is important in confirming the etiol. assocn. of the virus with disease as well as in understanding the pathogenesis of the disease. To our knowledge, there have been no comprehensive studies investigating viral infection at the cellular level in humans. Methods and Findings: We collected the largest series of fatal cases of SARS with autopsy material to date by merging the pathol. material from two regions involved in the 2003 worldwide SARS outbreak in Hong Kong, China, and Toronto, Canada. We developed a monoclonal antibody against the SARS-CoV nucleoprotein and used it together with in situ hybridization (ISH) to analyze the autopsy lung tissues of 32 patients with SARS from Hong Kong and Toronto. We compared the results of these assays with the pulmonary pathologies and the clin. course of illness for each patient. SARS-CoV nucleoprotein and RNA were detected by immunohistochem. and ISH, resp., primarily in alveolar pneumocytes and, less frequently, in macrophages. Such localization was detected in four of the seven patients who died within two weeks of illness onset, and in none of the 25 patients who died later than two weeks after symptom onset. Conclusions: The pulmonary alveolar epithelium is the chief target of SARS-CoV, with macrophages infected subsequently. Viral replication appears to be limited to the first two weeks after symptom onset, with little evidence of continued widespread replication after this period. If antiviral therapy is considered for future treatment, it should be focused on this two-week period of acute clin. disease.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 5 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Cited References

ACCESSION NUMBER: 2005:562710 CAPLUS
DOCUMENT NUMBER: 143:246447
TITLE: Use of monoclonal antibodies in blocking ELISA

detection of transmissible gastroenteritis virus in faeces of piglets

AUTHOR(S): Rodak, L.; Smid, B.; Nevorankova, Z.; Valicek, L.; Smitalova, R.

CORPORATE SOURCE: Veterinary Research Institute, Brno, Czech Rep.

SOURCE: Journal of Veterinary Medicine, Series B (2005), 52(3), 105-111
CODEN: JVMBE9; ISSN: 0931-1793

PUBLISHER: Blackwell Verlag GmbH

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Monoclonal antibodies (mAb) to the transmissible gastroenteritis virus (TGEV) nucleoprotein (N) and membrane protein (M) were prepd. and used for the comparative assessment of three blocking ELISA variants to detect TGEV. The competitive blocking ELISA format showed the highest sensitivity, allowing detection of 103 TCID50 TGEV/mL in culture medium. Ninety-nine porcine field fecal samples obtained from 37 herds affected with diarrhea were examd., and various TGEV levels were found in nine samples from six herds. However, only in three samples were significant TGEV concns. demonstrated. The relationship between incidence of TGEV gastroenteritis and the spread of porcine respiratory coronavirus infection in pig farms is discussed.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 6 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | String References

ACCESSION NUMBER: 2005:409560 CAPLUS

DOCUMENT NUMBER: 142:462283

TITLE: Monoclonal antibodies specific to SARS virus nucleoprotein for immunodiagnosis of SARS

INVENTOR(S): Uchida, Yoshiaki; Fujii, Nobuyuki; Kurano, Yoshihiro; Okada, Masahisa; Kogaki, Hiroyuki; Kido, Yasuji; Miyake, Kazushige

PATENT ASSIGNEE(S): Fujirebio Inc., Japan

SOURCE: PCT Int. Appl., 41 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005042579	A1	20050512	WO 2004-JP16099	20041029
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CN 1902230	A	20070124	CN 2004-80039648	20041029
IN 2006KN01457	A	20070504	IN 2006-KN1457	20060530
US 20080254440	A1	20081016	US 2007-577310	20070222

PRIORITY APPLN. INFO.:	JP 2003-373779	A	20031031
	JP 2004-34268	A	20040210
	WO 2004-JP16099	W	20041029

AB Provided are monoclonal antibodies specific to SARS virus nucleoprotein and hybridomas producing them. These monoclonal antibodies are labeled with enzyme and used for immunodiagnosis of SARS.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 7 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2004:872877 CAPLUS
DOCUMENT NUMBER: 141:378847
TITLE: Endogenous host elements or viral-based sequence elements for diagnosis, prognosis and therapy of viral infection, autoimmune disease and lymphoproliferative disease
INVENTOR(S): Hu, Yu-wen; Brown, Earl
PATENT ASSIGNEE(S): Canadian Blood Services, Can.
SOURCE: PCT Int. Appl., 174 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004090544	A2	20041021	WO 2004-CA544	20040413
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2522067	A1	20041021	CA 2004-2522067	20040413
EP 1625402	A2	20060215	EP 2004-726942	20040413
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR				
US 20060115875	A1	20060601	US 2005-248008	20051011

PRIORITY APPLN. INFO.:	US 2003-461137P	P	20030409
	US 2003-506779P	P	20030930
	WO 2004-CA544	W	20040413

AB A method of detecting, characterizing and treating viral infection, autoimmune disease and lymphoproliferative disease is provided. In particular, a strategy of mol. mimicry is provided for characterizing viral behavior and/or a predisposition for a given viral outcome in vivo. Novel compns. are also provided for detecting, characterizing and treating viral infections. The viral infection is caused by HCV, HIV, HTLV-1, HTLV-2, SARS-CoV, or a member of Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae, Poxviridae or Coronaviridae. The viral-based sequence element is e.g. an element of S protein sequence of an ORF1a protein sequence of SARS-CoV; a Gag, Pol or Env polyprotein of HTLV-1; a NS5A and E2 protein of HCV; bacterial virulence factor; human

endogenous retrovirus element; Peyer's patches virulence factor gipA; or an Ig selected from IgG, IgA, IgM, IgD or IgE. The treatment regime includes an anti-viral monoclonal or polyclonal antibody, or a compd. capable of binding epitope of the endogenous host element.

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Full Text | More Reference

ACCESSION NUMBER: 2004:541777 CAPLUS
DOCUMENT NUMBER: 141:222968
TITLE: Organ distribution of severe acute respiratory syndrome (SARS) associated coronavirus (SARS-CoV) in SARS patients: implications for pathogenesis and virus transmission pathways
AUTHOR(S): Ding, Yanqing; He, Li; Zhang, Qingling; Huang, Zhongxi; Che, Xiaoyan; Hou, Jinlin; Wang, Huijun; Shen, Hong; Qiu, Liwen; Li, Zhuguo; Geng, Jian; Cai, Junjie; Han, Huixia; Li, Xin; Kang, Wei; Weng, Desheng; Liang, Ping; Jiang, Shibo
CORPORATE SOURCE: Department of Pathology, Nan Fang Hospital, First Military Medical University, Guangzhou, Peop. Rep. China
SOURCE: Journal of Pathology (2004), 203(2), 622-630
CODEN: JPTLAS; ISSN: 0022-3417
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We previously identified the major pathol. changes in the respiratory and immune systems of patients who died of severe acute respiratory syndrome (SARS) but gained little information on the organ distribution of SARS-assocd. coronavirus (SARS-CoV). In the present study, we used a murine monoclonal antibody specific for SARS-CoV nucleoprotein, and probes specific for a SARS-CoV RNA polymerase gene fragment, for immunohistochem. and in situ hybridization, resp., to detect SARS-CoV systematically in tissues from patients who died of SARS. SARS-CoV was found in lung, trachea/bronchus, stomach, small intestine, distal convoluted renal tubule, sweat gland, parathyroid, pituitary, pancreas, adrenal gland, liver and cerebrum, but was not detected in esophagus, spleen, lymph node, bone marrow, heart, aorta, cerebellum, thyroid, testis, ovary, uterus or muscle. These results suggest that, in addn. to the respiratory system, the gastrointestinal tract and other organs with detectable SARS-CoV may also be targets of SARS-CoV infection. The pathol. changes in these organs may be caused directly by the cytopathic effect mediated by local replication of the SARS-CoV; or indirectly as a result of systemic responses to respiratory failure or the harmful immune response induced by viral infection. In addn. to viral spread through a respiratory route, SARS-CoV in the intestinal tract, kidney and sweat glands may be excreted via feces, urine and sweat, thereby leading to virus transmission. This study provides important information for understanding the pathogenesis of SARS-CoV infection and sheds light on possible virus transmission pathways. This data will be useful for designing new strategies for prevention and treatment of SARS.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 9 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | More Reference

ACCESSION NUMBER: 2004:539287 CAPLUS
DOCUMENT NUMBER: 141:275951

TITLE: Development and characterisation of neutralising monoclonal antibody to the SARS-coronavirus
AUTHOR(S): Berry, Jody D.; Jones, Steven; Drebot, Michael A.; Andonov, Anton; Sabara, Marta; Yuan, Xin Y.; Weingartl, Hana; Fernando, Lisa; Marszal, Peter; Gren, Jason; Nicolas, Brigitte; Andonova, Maya; Ranada, Francesca; Gubbins, Michael J.; Ball, T. Blake; Kitching, Paul; Li, Yan; Kabani, Amin; Plummer, Frank
CORPORATE SOURCE: Department of Medical Microbiology, National Centre for Foreign Animal Disease, CFIA, University of Manitoba, Winnipeg, Can.
SOURCE: Journal of Virological Methods (2004), 120(1), 87-96 CODEN: JVMEDH; ISSN: 0166-0934
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB There is a global need to elucidate protective antigens expressed by the SARS-coronavirus (SARS-CoV). Monoclonal antibody reagents that recognize specific antigens on SARS-CoV are needed urgently. In this report, the development and immunochem. characterization of a panel of murine monoclonal antibodies (mAbs) against the SARS-CoV is presented, based upon their specificity, binding requirements, and biol. activity. Initial screening by ELISA, using highly purified virus as the coating antigen, resulted in the selection of 103 mAbs to the SARS virus. Subsequent screening steps reduced this panel to seventeen IgG mAbs. A single mAb, F26G15, is specific for the nucleoprotein as seen in Western immunoblot while five other mAbs react with the Spike protein. Two of these Spike-specific mAbs demonstrate the ability to neutralize SARS-CoV in vitro while another four Western immunoblot-neg. mAbs also neutralize the virus. The utility of these mAbs for diagnostic development is demonstrated. Antibody from convalescent SARS patients, but not normal human serum, is also shown to specifically compete off binding of mAbs to whole SARS-CoV. These studies highlight the importance of using standardized assays and reagents. These mAbs will be useful for the development of diagnostic tests, studies of SARS-CoV pathogenesis and vaccine development.

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 10 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Other References

ACCESSION NUMBER: 2001:48484 CAPLUS
DOCUMENT NUMBER: 134:219537
TITLE: The membrane M protein carboxy terminus binds to transmissible gastroenteritis coronavirus core and contributes to core stability
AUTHOR(S): Escors, David; Ortego, Javier; Laude, Hubert; Enjuanes, Luis
CORPORATE SOURCE: Department of Molecular and Cell Biology, Centro Nacional de Biotecnologia, CSIC, Madrid, 28049, Spain
SOURCE: Journal of Virology (2001), 75(3), 1312-1324 CODEN: JOVIAM; ISSN: 0022-538X
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The architecture of transmissible gastroenteritis coronavirus includes three different structural levels, the envelope, an internal core, and the nucleocapsid that is released when the core is disrupted. Starting from purified virions, core structures have been reproducibly isolated as

independent entities. The cores were stabilized at basic pH and by the presence of divalent cations, with Mg2+ ions more effectively contributing to core stability. Core structures showed high resistance to different concns. of detergents, reducing agents, and urea and low concns. of monovalent ions (<200 mM). Cores were composed of the nucleoprotein, RNA, and the C domain of the membrane (M) protein. At high salt concns. (200 to 300 mM), the M protein was no longer assocd. with the nucleocapsid, which resulted in destruction of the core structure. A specific ionic interaction between the M protein carboxy terminus and the nucleocapsid was demonstrated using three complementary approaches: (i) a binding assay performed between a collection of M protein amino acid substitution or deletion mutants and purified nucleocapsids that led to the identification of a 16-amino-acid (aa) domain (aa 237 to 252) as being responsible for binding the M protein to the nucleocapsid; (ii) the specific inhibition of this binding by monoclonal antibodies (MAbs) binding to a carboxy-terminal M protein domain close to the indicated peptide but not by MAbs specific for the M protein amino terminus; and (iii) a 26-residue peptide, including the predicted sequence (aa 237 to 252), which specifically inhibited the binding. Direct binding of the M protein to the nucleoprotein was predicted, since degrdn. of the exposed RNA by RNase treatment did not affect the binding. It is proposed that the M protein is embedded within the virus membrane and that the C region, exposed to the interior face of the virion in a population of these mols., interacts with the nucleocapsid to which it is anchored, forming the core. Only the C region of the M protein is part of the core.

REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 11 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | RHCA References

ACCESSION NUMBER: 1999:336041 CAPLUS
DOCUMENT NUMBER: 131:156705
TITLE: Production, characterization, and uses of monoclonal antibodies against recombinant nucleoprotein of elk coronavirus
AUTHOR(S): Daginakatte, Girish C.; Chard-Bergstrom, Cindy; Andrews, Gordon A.; Kapil, Sanjay
CORPORATE SOURCE: Department of Diagnostic Medicine-Pathobiology, College of Veterinary Medicine, Manhattan, KS, 66506, USA
SOURCE: Clinical and Diagnostic Laboratory Immunology (1999), 6(3), 341-344
CODEN: CDIMEN; ISSN: 1071-412X
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB This is the first report of the prodn. of monoclonal antibodies against elk coronavirus. The nucleoprotein gene of elk coronavirus was amplified by PCR and was cloned and expressed in a prokaryotic expression vector. Recombinant nucleocapsid protein was used to immunize mice for the prodn. of hybridomas. Twelve hybridomas that produced monoclonal antibodies against the nucleocapsid protein of elk coronavirus were selected by an indirect fluorescent-antibody test, an ELISA, and a Western blot assay. Ten of the monoclonal antibodies were of the IgG1 isotype, one was IgG2a, and one was IgM. All had kappa light chains. By immunohistochem. four monoclonal antibodies detected bovine coronavirus and elk coronavirus in formalin-fixed intestinal tissues. Anti-nucleoprotein monoclonal antibodies were better at ruminant coronavirus detection than the anti-spike protein monoclonal

antibodies. Because nucleoprotein is a more abundant antigen than spike protein in infected cells, this was not an unexpected finding.
REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 12 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | String References

ACCESSION NUMBER: 1997:723088 CAPLUS
DOCUMENT NUMBER: 128:58017
ORIGINAL REFERENCE NO.: 128:11239a,11242a
TITLE: Isolation and characterization of a coronavirus from elk calves with diarrhea
AUTHOR(S): Majhdi, F.; Minocha, H. C.; Kapil, S.
CORPORATE SOURCE: Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS, 66506, USA
SOURCE: Journal of Clinical Microbiology (1997), 35(11), 2937-2942
CODEN: JCMIDW; ISSN: 0095-1137
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB This is the first report of the isolation of a coronavirus from elk calves. Two fecal samples from elk calves with diarrhea were shown to be pos. for coronavirus-like particles by electron microscopy, and the particles were propagated in the human rectal tumor-18 cell line. After 24 h, syncytia were obsd., and cell culture supernatants from both samples showed hemagglutinating activity with mouse erythrocytes. Cells infected with both elk coronavirus (ECV) isolates reacted with Z3A5, a monoclonal antibody against the spike protein of bovine coronavirus (BCV), on an indirect fluorescent antibody test. The protein profiles of both ECV isolates were similar to that of BCV as detd. by sodium dodecyl sulfate-polyacrylamide gel electrophoresis anal. On Northern blot anal., the transcriptional pattern of ECV was typical of coronaviruses, with a nested set of transcripts with common 3' end sequences. Based on a published nucleoprotein gene sequence for BCV (Mebus isolate), we arbitrarily designed two primers for amplification by PCR. After cloning, the nucleoprotein was sequenced and a high degree of homol. (99%) between the nucleoprotein gene sequences of ECV and BCV was obsd. Thus, ECV is closely related genetically and antigenically to BCV and will be a new member of antigenic group 2 of the mammalian coronaviruses, which possess hemagglutinin-esterase protein.

L20 ANSWER 13 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | String References

ACCESSION NUMBER: 1995:945210 CAPLUS
DOCUMENT NUMBER: 124:47424
ORIGINAL REFERENCE NO.: 124:8827a,8830a
TITLE: Experimental evidence of recombination in coronavirus infectious bronchitis virus
AUTHOR(S): Kottier, Sanneke A.; Cavanagh, David; Britton, Paul
CORPORATE SOURCE: Division Molecular Biology, Institute Animal Health, Compton, Newbury, Berkshire, RG20 7NN, UK
SOURCE: Virology (1995), 213(2), 569-80
CODEN: VIRLAX; ISSN: 0042-6822
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Embryonated eggs were coinfected with two strains of the coronavirus avian infectious bronchitis virus (IBV), IBV-Beaudette and IBV-M41, to investigate whether recombination between the two strains would occur. Virions were isolated from the allantoic fluid of the coinfected eggs and putative hybrid RNAs were detected by polymerase chain reaction (PCR), using strain-specific oligonucleotides. PCR products, of the expected sizes, were obtained as predicted from potential recombination events between the nucleoprotein (N) gene and the 3'-untranslated region of the two IBV genomes. Sequencing confirmed that they corresponded to hybrid RNAs. Virus produced as a result of the mixed infection was treated with an M41-specific neutralizing monoclonal and passaged in Vero cells, in which IBV-beaudette, but not IBV-M41, replicated. Hybrid RNA was still detectable after three serial passages. Since no IBV-M41 was detectable this confirmed that infectious recombinant genomes had been produced in the embryonated eggs. These findings not only support the circumstantial evidence, from sequencing studies of IBV field strains, that recombination occurs during replication of IBV and contributes to the diversity of IBV, but also show that coronavirus RNA recombination is not limited to mouse hepatitis virus.

L20 ANSWER 14 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Other References

ACCESSION NUMBER: 1991:533524 CAPLUS
DOCUMENT NUMBER: 115:133524
ORIGINAL REFERENCE NO.: 115:22845a,22848a
TITLE: Comparison of bovine coronavirus (BCV) antigens: monoclonal antibodies to the spike glycoprotein distinguish between vaccine and wild-type strains
AUTHOR(S): Hussain, Khalid A.; Storz, Johannes; Kousoulas, Konstantin G.
CORPORATE SOURCE: Sch. Vet. Med., Louisiana State Univ., Baton Rouge, LA, 70803, USA
SOURCE: Virology (1991), 183(1), 442-5
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Monoclonal antibodies (MAbs) against two major structural proteins of the cell-adapted Mebus strain of bovine coronavirus (BCV-L9) were produced and characterized. Seven MAbs reacted with the peplomeric glycoprotein, gp100/S, while three MAbs reacted with the nucleoprotein p53/N in Western blot anal. of BCV polypeptides. MAbs to gp100/S reacted with discontinuous epitopes of gp100/S in Westerns under mild but not under std. denaturing conditions. In contrast, MAbs to p53/N reacted in both types of Westerns, and those epitopes were thus continuous. MAbs to p53/N failed to neutralize BCV infectivity, while 4 MAbs to gp100/S neutralized BCV effectively. Cross reactivity of MAbs to gp100/S specified by five virulent wild-type strains and two high passage, cell-culture-adapted strains in mildly denaturing Westerns and neutralization assays indicated that two epitopes were conserved in all seven strains, while two epitopes of the avirulent strains were not detected in the wild-type strains. Non-neutralizing MAbs of gp100/S reacted with all seven strains in Westerns with the exception of one MAb that was specific for the highly cell-adapted strain BCV-L9.

L20 ANSWER 15 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Other References

ACCESSION NUMBER: 1988:470029 CAPLUS
DOCUMENT NUMBER: 109:70029

ORIGINAL REFERENCE NO.: 109:11669a,11672a
TITLE: Antigenic differentiation between transmissible gastroenteritis virus of swine and a related porcine respiratory coronavirus
AUTHOR(S): Callebaut, P.; Correa, I.; Pensaert, M.; Jimenez, G.; Enjuanes, L.
CORPORATE SOURCE: Fac. Vet. Med., State Univ. Gent, Ghent, B-9000, Belg.
SOURCE: Journal of General Virology (1988), 69(7), 1725-30
CODEN: JGVIAY; ISSN: 0022-1317
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The antigenic relationship between isolated porcine respiratory coronavirus (TLM 83) and transmissible gastroenteritis (TGE) virus of swine was studied by neutralization, immunoblotting, and RIA, using TGE virus-specific monoclonal antibodies (MAbs) and polyclonal antibodies specific for both viruses. A complete two-way neutralization activity between the two viruses was found. Immunoblotting revealed cross-reactions between TLM 83 and TGE virus antigens at the level of the envelope protein (E1), the nucleoprotein (N), and the peplomer protein (E2). By virus neutralization assays and RIA with TGE virus-specific MAbs, the presence of similar epitopes in the E1 and N proteins and in the neutralization-mediating antigenic site of the E2 protein were demonstrated. E2 protein-specific MAbs, without neutralizing activity and reacting with antigenic sites B, C, and D (previously defined), failed to recognize TLM 83. These results indicated a close antigenic relationship and structural similarity between TLM 83 and TGE viruses and also suggested potential ways of differentiating between the two viruses.

L20 ANSWER 16 OF 16 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | RIA | References

ACCESSION NUMBER: 1984:3195 CAPLUS
DOCUMENT NUMBER: 100:3195
ORIGINAL REFERENCE NO.: 100:551a,554a
TITLE: Synthesis and subcellular localization of the murine coronavirus nucleocapsid protein
AUTHOR(S): Stohlman, Stephen A.; Fleming, John O.; Patton, Chris D.; Lai, Michael M. C.
CORPORATE SOURCE: Sch. Med., Univ. South. California, Los Angeles, CA, 90033, USA
SOURCE: Virology (1983), 130(2), 527-32
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The synthesis and processing of the nucleocapsid protein (pp60) of the JHM strain of murine coronaviruses were examd. Pulse-chase expts. showed that pp60 was synthesized initially as a protein of mol. wt. ~57,000 (p57). Immunopptn. using mouse anti-JHMV antiserum indicated that p57 was virus specific. Immunopptn. with monoclonal antibodies specific for pp60 showed that p57 was antigenically related to pp60 and was not phosphorylated, whereas the intracellular protein that comigrated with the virion nucleocapsid protein, pp60, was phosphorylated. The p57 was found exclusively in the cytosol whereas the majority of pp60 was assocd. with the membrane fraction but pp60 was not an integral membrane protein.

=> D L16 TRIE ABS 1-8

L16 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2007:147094 CAPLUS
DOCUMENT NUMBER: 147:46687
TITLE: Cloning, expressing and antigenicity analysis of nucleocapsid proteins of SARS-CoV, HCoV-229E and OC43
AUTHOR(S): Che, Xiaoyan; Liao, Zhiyong; Wang, Yadi; Qiu, Liwen; Wen, Kun; Pan, Yuxian; Xu, Hua; Mei, Yabo; Hao, Wei; Ding, Yanqing
CORPORATE SOURCE: Zhujiang Hospital, Southern Medical University, Guangzhou, 510282, Peop. Rep. China
SOURCE: Zhonghua Weishengwuxue He Mianyixue Zazhi (2005), 25(9), 711-715
CODEN: ZWMZDP; ISSN: 0254-5101
PUBLISHER: Beijing Shengwu Zhipin Yanjiuso
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB A recombinant nucleocapsid (N) protein of SARS-CoV, HCoV-229E and HCoV-OC43, was obtained resp. to study antigenic relationships of N proteins between SARS-CoV and human coronaviruses 229E and OC43. The genes encoding the full-length of N proteins from SARS-CoV, HCoV-229E and HCoV-OC43 were amplified by RT-PCR and cloned into the prokaryotic expression vector pQE30. The His6-tagged N proteins were expressed in the M15 strain and further purified with affinity chromatog. The antigenicity of N proteins was analyzed by Western blot and immunofluorescence assay. The N genes of 1281, 1182 and 1359 bp from SARS-CoV, HCoV-229E and HCoV-OC43, resp. were amplified with their corresponding primer pairs. The recombinant plasmids were sequenced, and they were all in frame with sequences matching those for the N genes of the three coronaviruses. The expressed recombinant His6-tagged N proteins were identified by Western blot assay with anti-His tag monoclonal antibody. The immunoreactive protein bands with expected sizes were 47 kDa, 44 kDa and 50 kDa from SARS-CoV, HCoV-229E and HCoV-OC43, resp. The nucleocapsid proteins of SARS-CoV, HCoV-229E and HCoV-OC43 strongly and specifically reacted with the virus specific rabbit serum and with the nucleoprotein specific murine serum. No cross-reactivity was found among the nucleocapsid proteins of SARS-CoV, HCoV-229E and HCoV-OC43. The immunogenic nucleocapsid recombinant proteins from SARS-CoV, HCoV-229E and HCoV-OC43 were obtained. There was no antigenic relationship among the three N proteins.

L16 ANSWER 2 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2006:1263772 CAPLUS
DOCUMENT NUMBER: 146:137159
TITLE: Coronavirus nucleocapsid protein is an RNA chaperone
AUTHOR(S): Zuniga, Sonia; Sola, Isabel; Moreno, Jose L.; Sabella, Patricia; Plana-Duran, Juan; Enjuanes, Luis
CORPORATE SOURCE: Centro Nacional de Biotecnologia, CSIC, Department of Molecular and Cell Biology, Campus Universidad Autonoma, Madrid, 28049, Spain
SOURCE: Virology (2007), 357(2), 215-227
CODEN: VIRLAX; ISSN: 0042-6822
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB RNA chaperones are nonspecific nucleic acid binding proteins with long disordered regions that help RNA mols. to adopt its functional conformation. Coronavirus nucleoproteins (N) are nonspecific

RNA-binding proteins with long disordered regions. Therefore, we investigated whether transmissible gastroenteritis coronavirus (TGEV) N protein was an RNA chaperone. Purified N protein enhanced hammerhead ribozyme self-cleavage and nucleic acids annealing, which are properties that define RNA chaperones. In contrast, another RNA-binding protein, PTB, did not show these activities. N protein chaperone activity was blocked by specific monoclonal antibodies. Therefore, it was concluded that TGEV N protein is an RNA chaperone. In addn., we have shown that purified severe acute respiratory syndrome (SARS)-CoV N protein also has RNA chaperone activity. In silico predictions of disordered domains showed a similar pattern for all coronavirus N proteins evaluated. Altogether, these data led us to suggest that all coronavirus N proteins might be RNA chaperones.

REFERENCE COUNT: 83 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | More References

ACCESSION NUMBER: 2006:1139612 CAPLUS
DOCUMENT NUMBER: 146:140843
TITLE: Antigenic and cellular localisation analysis of the severe acute respiratory syndrome coronavirus nucleocapsid protein using monoclonal antibodies
AUTHOR(S): Bussmann, Bianca M.; Reiche, Sven; Jacob, Lotta H.; Braun, Jan Matthias; Jassoy, Christian
CORPORATE SOURCE: Institute of Virology, University of Leipzig, Leipzig, 04103, Germany
SOURCE: Virus Research (2006), 122(1-2), 119-126
CODEN: VIREDF; ISSN: 0168-1702
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A member of the family of coronaviruses has previously been identified as the cause of the severe acute respiratory syndrome (SARS). In this study, several monoclonal antibodies against the nucleocapsid protein have been generated to examine distribution of the nucleocapsid in virus-infected cells and to study antigenic regions of the protein. Confocal microscopic anal. identified nucleocapsids packaged in vesicles in the perinuclear area indicating viral synthesis at the endoplasmic reticulum and Golgi app. The monoclonal antibodies bound to the central and carboxyterminal half of the nucleocapsid protein indicating prominent exposure and immunogenicity of this part of the protein. Antibodies recognized both linear and conformational epitopes. Predictions of antigenicity using amt.. modeling based on hydrophobicity anal. of SARS nucleoprotein could not be confirmed fully. Antibody binding to discontinuous peptides provides evidence that amino acids 274-283 and 373-382 assemble to a structural unit particularly rich in basic amino acids. In addn., amino acids 286-295, 316-325 and 361-367 that represent the epitope recognized by monoclonal antibody 6D11C1 converge indicating a well-structured C-terminal region of the SARS virus nucleocapsid protein and functional relation of the peptide regions involved. Alternatively, dimerization of the nucleocapsid protein may result in juxtaposition of the amino acid sequences 316-325 and 361-367 on one nucleoprotein mol. to amino acid 286-295 on the second peptide. The monoclonal antibodies will be available to assess antigenicity and immunol. variabilities between different SARS CoV strains.

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2006:236188 CAPLUS
DOCUMENT NUMBER: 145:185561
TITLE: Time course and cellular localization of SARS-CoV nucleoprotein and RNA in lungs from fatal cases of SARS
AUTHOR(S): Nicholls, John M.; Butany, Jagdish; Poon, Leo L. M.; Chan, Kwok H.; Beh, Swan Lip; Poutanen, Susan; Peiris, J. S. Malik; Wong, Maria
CORPORATE SOURCE: Department of Pathology, The University of Hong Kong, Pok Fu Lam, Hong Kong SAR, Peop. Rep. China
SOURCE: PLoS Medicine (2006), 3(2), 222-229
CODEN: PMLEAC; ISSN: 1549-1277
URL: http://medicine.plosjournals.org/archive/1549-1676/3/2/pdf/10.1371_1549-1676_3_2_complete.pdf
PUBLISHER: Public Library of Science
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English

AB Background: Cellular localization of severe acute respiratory syndrome coronavirus (SARS-CoV) in the lungs of patients with SARS is important in confirming the etiol. assocn. of the virus with disease as well as in understanding the pathogenesis of the disease. To our knowledge, there have been no comprehensive studies investigating viral infection at the cellular level in humans. Methods and Findings: We collected the largest series of fatal cases of SARS with autopsy material to date by merging the pathol. material from two regions involved in the 2003 worldwide SARS outbreak in Hong Kong, China, and Toronto, Canada. We developed a monoclonal antibody against the SARS-CoV nucleoprotein and used it together with in situ hybridization (ISH) to analyze the autopsy lung tissues of 32 patients with SARS from Hong Kong and Toronto. We compared the results of these assays with the pulmonary pathologies and the clin. course of illness for each patient. SARS-CoV nucleoprotein and RNA were detected by immunohistochem. and ISH, resp., primarily in alveolar pneumocytes and, less frequently, in macrophages. Such localization was detected in four of the seven patients who died within two weeks of illness onset, and in none of the 25 patients who died later than two weeks after symptom onset. Conclusions: The pulmonary alveolar epithelium is the chief target of SARS-CoV, with macrophages infected subsequently. Viral replication appears to be limited to the first two weeks after symptom onset, with little evidence of continued widespread replication after this period. If antiviral therapy is considered for future treatment, it should be focused on this two-week period of acute clin. disease.

REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2005:409560 CAPLUS
DOCUMENT NUMBER: 142:462283
TITLE: Monoclonal antibodies specific to SARS virus nucleoprotein for immunodiagnosis of SARS
INVENTOR(S): Uchida, Yoshiaki; Fujii, Nobuyuki; Kurano, Yoshihiro; Okada, Masahisa; Kogaki, Hiroyuki; Kido, Yasuji; Miyake, Kazushige
PATENT ASSIGNEE(S): Fujirebio Inc., Japan
SOURCE: PCT Int. Appl., 41 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005042579	A1	20050512	WO 2004-JP16099	20041029
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CN 1902230	A	20070124	CN 2004-80039648	20041029
IN 2006KN01457	A	20070504	IN 2006-KN1457	20060530
US 20080254440	A1	20081016	US 2007-577310	20070222
PRIORITY APPLN. INFO.:			JP 2003-373779 A	20031031
			JP 2004-34268 A	20040210
			WO 2004-JP16099 W	20041029

AB Provided are monoclonal antibodies specific to SARS virus nucleoprotein and hybridomas producing them. These monoclonal antibodies are labeled with enzyme and used for immunodiagnosis of SARS.
REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN
Full Text | Citing References

ACCESSION NUMBER: 2004:872877 CAPLUS
DOCUMENT NUMBER: 141:378847
TITLE: Endogenous host elements or viral-based sequence elements for diagnosis, prognosis and therapy of viral infection, autoimmune disease and lymphoproliferative disease
INVENTOR(S): Hu, Yu-wen; Brown, Earl
PATENT ASSIGNEE(S): Canadian Blood Services, Can.
SOURCE: PCT Int. Appl., 174 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004090544	A2	20041021	WO 2004-CA544	20040413
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ,				

BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

CA 2522067	A1	20041021	CA 2004-2522067	20040413
EP 1625402	A2	20060215	EP 2004-726942	20040413
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR				
US 20060115875	A1	20060601	US 2005-248008	20051011
PRIORITY APPLN. INFO.:			US 2003-461137P	P 20030409
			US 2003-506779P	P 20030930
			WO 2004-CA544	W 20040413

AB A method of detecting, characterizing and treating viral infection, autoimmune disease and lymphoproliferative disease is provided. In particular, a strategy of mol. mimicry is provided for characterizing viral behavior and/or a predisposition for a given viral outcome in vivo. Novel compns. are also provided for detecting, characterizing and treating viral infections. The viral infection is caused by HCV, HIV, HTLV-1, HTLV-2, SARS-CoV, or a member of Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae, Poxviridae or Coronaviridae. The viral-based sequence element is e.g. an element of S protein sequence of an ORF1a protein sequence of SARS-CoV; a Gag, Pol or Env polyprotein of HTLV-1; a NS5A and E2 protein of HCV; bacterial virulence factor; human endogenous retrovirus element; Peyer's patches virulence factor gipA; or an Ig selected from IgG, IgA, IgM, IgD or IgE. The treatment regime includes an anti-viral monoclonal or polyclonal antibody, or a compd. capable of binding epitope of the endogenous host element.

L16 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | RN's References

ACCESSION NUMBER:	2004:541777 CAPLUS
DOCUMENT NUMBER:	141:222968
TITLE:	Organ distribution of severe acute respiratory syndrome (SARS) associated coronavirus (SARS-CoV) in SARS patients: implications for pathogenesis and virus transmission pathways
AUTHOR(S):	Ding, Yanqing; He, Li; Zhang, Qingling; Huang, Zhongxi; Che, Xiaoyan; Hou, Jinlin; Wang, Huijun; Shen, Hong; Qiu, Liwen; Li, Zhuguo; Geng, Jian; Cai, Junjie; Han, Huixia; Li, Xin; Kang, Wei; Weng, Desheng; Liang, Ping; Jiang, Shibo
CORPORATE SOURCE:	Department of Pathology, Nan Fang Hospital, First Military Medical University, Guangzhou, Peop. Rep. China
SOURCE:	Journal of Pathology (2004), 203(2), 622-630 CODEN: JPTLAS; ISSN: 0022-3417
PUBLISHER:	John Wiley & Sons Ltd.
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB We previously identified the major pathol. changes in the respiratory and immune systems of patients who died of severe acute respiratory syndrome (SARS) but gained little information on the organ distribution of SARS-assocd. coronavirus (SARS-CoV). In the present study, we used a murine monoclonal antibody specific for SARS-CoV nucleoprotein, and probes specific for a SARS-CoV RNA polymerase gene fragment, for immunohistochem. and in situ hybridization, resp., to detect SARS-CoV systematically in tissues from patients who died of SARS. SARS-CoV was found in lung, trachea/bronchus, stomach, small intestine, distal convoluted renal tubule, sweat gland, parathyroid, pituitary, pancreas,

adrenal gland, liver and cerebrum, but was not detected in esophagus, spleen, lymph node, bone marrow, heart, aorta, cerebellum, thyroid, testis, ovary, uterus or muscle. These results suggest that, in addn. to the respiratory system, the gastrointestinal tract and other organs with detectable SARS-CoV may also be targets of SARS-CoV infection. The pathol. changes in these organs may be caused directly by the cytopathic effect mediated by local replication of the SARS-CoV; or indirectly as a result of systemic responses to respiratory failure or the harmful immune response induced by viral infection. In addn. to viral spread through a respiratory route, SARS-CoV in the intestinal tract, kidney and sweat glands may be excreted via feces, urine and sweat, thereby leading to virus transmission. This study provides important information for understanding the pathogenesis of SARS-CoV infection and sheds light on possible virus transmission pathways. This data will be useful for designing new strategies for prevention and treatment of SARS.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Cited References

ACCESSION NUMBER: 2004:539287 CAPLUS
DOCUMENT NUMBER: 141:275951
TITLE: Development and characterisation of neutralising monoclonal antibody to the SARS-coronavirus
AUTHOR(S): Berry, Jody D.; Jones, Steven; Drebot, Michael A.; Andonov, Anton; Sabara, Marta; Yuan, Xin Y.; Weingartl, Hana; Fernando, Lisa; Marszal, Peter; Gren, Jason; Nicolas, Brigitte; Andonova, Maya; Ranada, Francesca; Gubbins, Michael J.; Ball, T. Blake; Kitching, Paul; Li, Yan; Kabani, Amin; Plummer, Frank
CORPORATE SOURCE: Department of Medical Microbiology, National Centre for Foreign Animal Disease, CFIA, University of Manitoba, Winnipeg, Can.
SOURCE: Journal of Virological Methods (2004), 120(1), 87-96 CODEN: JVMEDH; ISSN: 0166-0934
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB There is a global need to elucidate protective antigens expressed by the SARS-coronavirus (SARS-CoV). Monoclonal antibody reagents that recognize specific antigens on SARS-CoV are needed urgently. In this report, the development and immunochem. characterization of a panel of murine monoclonal antibodies (mAbs) against the SARS-CoV is presented, based upon their specificity, binding requirements, and biol. activity. Initial screening by ELISA, using highly purified virus as the coating antigen, resulted in the selection of 103 mAbs to the SARS virus. Subsequent screening steps reduced this panel to seventeen IgG mAbs. A single mAb, F26G15, is specific for the nucleoprotein as seen in Western immunoblot while five other mAbs react with the Spike protein. Two of these Spike-specific mAbs demonstrate the ability to neutralize SARS-CoV in vitro while another four Western immunoblot-neg. mAbs also neutralize the virus. The utility of these mAbs for diagnostic development is demonstrated. Antibody from convalescent SARS patients, but not normal human serum, is also shown to specifically compete off binding of mAbs to whole SARS-CoV. These studies highlight the importance of using standardized assays and reagents. These mAbs will be useful for the development of diagnostic tests, studies of SARS-CoV pathogenesis and vaccine development.

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> D L15 IBIB ABS 1-15

L15 ANSWER 1 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2007:147094 CAPLUS
DOCUMENT NUMBER: 147:46687
TITLE: Cloning, expressing and antigenicity analysis of nucleocapsid proteins of SARS-CoV, HCoV-229E and OC43
AUTHOR(S): Che, Xiaoyan; Liao, Zhiyong; Wang, Yadi; Qiu, Liwen; Wen, Kun; Pan, Yuxian; Xu, Hua; Mei, Yabo; Hao, Wei; Ding, Yanqing
CORPORATE SOURCE: Zhujiang Hospital, Southern Medical University, Guangzhou, 510282, Peop. Rep. China
SOURCE: Zhonghua Weishengwuxue He Mianyixue Zazhi (2005), 25(9), 711-715
CODEN: ZWMZDP; ISSN: 0254-5101
PUBLISHER: Beijing Shengwu Zhipin Yanjiuso
DOCUMENT TYPE: Journal
LANGUAGE: Chinese

AB A recombinant nucleocapsid (N) protein of SARS-CoV, HCoV-229E and HCoV-OC43, was obtained resp. to study antigenic relationships of N proteins between SARS-CoV and human coronaviruses 229E and OC43. The genes encoding the full-length of N proteins from SARS-CoV, HCoV-229E and HCoV-OC43 were amplified by RT-PCR and cloned into the prokaryotic expression vector pQE30. The His6-tagged N proteins were expressed in the M15 strain and further purified with affinity chromatog. The antigenicity of N proteins was analyzed by Western blot and immunofluorescence assay. The N genes of 1281, 1182 and 1359 bp from SARS-CoV, HCoV-229E and HCoV-OC43, resp. were amplified with their corresponding primer pairs. The recombinant plasmids were sequenced, and they were all in frame with sequences matching those for the N genes of the three coronaviruses. The expressed recombinant His6-tagged N proteins were identified by Western blot assay with anti-His tag monoclonal antibody. The immunoreactive protein bands with expected sizes were 47 kDa, 44 kDa and 50 kDa from SARS-CoV, HCoV-229E and HCoV-OC43, resp. The nucleocapsid proteins of SARS-CoV, HCoV-229E and HCoV-OC43 strongly and specifically reacted with the virus specific rabbit serum and with the nucleoprotein specific murine serum. No cross-reactivity was found among the nucleocapsid proteins of SARS-CoV, HCoV-229E and HCoV-OC43. The immunogenic nucleocapsid recombinant proteins from SARS-CoV, HCoV-229E and HCoV-OC43 were obtained. There was no antigenic relationship among the three N proteins.

L15 ANSWER 2 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2006:1263772 CAPLUS
DOCUMENT NUMBER: 146:137159
TITLE: Coronavirus nucleocapsid protein is an RNA chaperone
AUTHOR(S): Zuniga, Sonia; Sola, Isabel; Moreno, Jose L.; Sabella, Patricia; Plana-Duran, Juan; Enjuanes, Luis
CORPORATE SOURCE: Centro Nacional de Biotecnologia, CSIC, Department of Molecular and Cell Biology, Campus Universidad Autonoma, Madrid, 28049, Spain
SOURCE: Virology (2007), 357(2), 215-227
CODEN: VIRLAX; ISSN: 0042-6822

PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB RNA chaperones are nonspecific nucleic acid binding proteins with long disordered regions that help RNA mols. to adopt its functional conformation. Coronavirus nucleoproteins (N) are nonspecific RNA-binding proteins with long disordered regions. Therefore, we investigated whether transmissible gastroenteritis coronavirus (TGEV) N protein was an RNA chaperone. Purified N protein enhanced hammerhead ribozyme self-cleavage and nucleic acids annealing, which are properties that define RNA chaperones. In contrast, another RNA-binding protein, PTB, did not show these activities. N protein chaperone activity was blocked by specific monoclonal antibodies. Therefore, it was concluded that TGEV N protein is an RNA chaperone. In addn., we have shown that purified severe acute respiratory syndrome (SARS)-CoV N protein also has RNA chaperone activity. In silico predictions of disordered domains showed a similar pattern for all coronavirus N proteins evaluated. Altogether, these data led us to suggest that all coronavirus N proteins might be RNA chaperones.
REFERENCE COUNT: 83 THERE ARE 83 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 3 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2006:1139612 CAPLUS
DOCUMENT NUMBER: 146:140843
TITLE: Antigenic and cellular localisation analysis of the severe acute respiratory syndrome coronavirus nucleocapsid protein using monoclonal antibodies
AUTHOR(S): Bussmann, Bianca M.; Reiche, Sven; Jacob, Lotta H.; Braun, Jan Matthias; Jassoy, Christian
CORPORATE SOURCE: Institute of Virology, University of Leipzig, Leipzig, 04103, Germany
SOURCE: Virus Research (2006), 122(1-2), 119-126
CODEN: VIREDF; ISSN: 0168-1702
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A member of the family of coronaviruses has previously been identified as the cause of the severe acute respiratory syndrome (SARS). In this study, several monoclonal antibodies against the nucleocapsid protein have been generated to examine distribution of the nucleocapsid in virus-infected cells and to study antigenic regions of the protein. Confocal microscopic anal. identified nucleocapsids packaged in vesicles in the perinuclear area indicating viral synthesis at the endoplasmic reticulum and Golgi app. The monoclonal antibodies bound to the central and carboxyterminal half of the nucleocapsid protein indicating prominent exposure and immunogenicity of this part of the protein. Antibodies recognized both linear and conformational epitopes. Predictions of antigenicity using amt.. modeling based on hydrophobicity anal. of SARS nucleoprotein could not be confirmed fully. Antibody binding to discontinuous peptides provides evidence that amino acids 274-283 and 373-382 assemble to a structural unit particularly rich in basic amino acids. In addn., amino acids 286-295, 316-325 and 361-367 that represent the epitope recognized by monoclonal antibody 6D11C1 converge indicating a well-structured C-terminal region of the SARS virus nucleocapsid protein and functional relation of the peptide regions involved. Alternatively, dimerization of the nucleocapsid protein may result in juxtaposition of the amino acid sequences 316-325 and 361-367 on

one nucleoprotein mol. to amino acid 286-295 on the second peptide. The monoclonal antibodies will be available to assess antigenicity and immunol. variabilities between different SARS CoV strains.
REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN
Full Text | Cited References

ACCESSION NUMBER: 2006:236188 CAPLUS
DOCUMENT NUMBER: 145:185561
TITLE: Time course and cellular localization of SARS-CoV nucleoprotein and RNA in lungs from fatal cases of SARS
AUTHOR(S): Nicholls, John M.; Butany, Jagdish; Poon, Leo L. M.; Chan, Kwok H.; Beh, Swan Lip; Poutanen, Susan; Peiris, J. S. Malik; Wong, Maria
CORPORATE SOURCE: Department of Pathology, The University of Hong Kong, Pok Fu Lam, Hong Kong SAR, Peop. Rep. China
SOURCE: PLoS Medicine (2006), 3(2), 222-229
CODEN: PMLEAC; ISSN: 1549-1277
URL: http://medicine.plosjournals.org/archive/1549-1676/3/2/pdf/10.1371_1549-1676_3_2_complete.pdf
PUBLISHER: Public Library of Science
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English
AB Background: Cellular localization of severe acute respiratory syndrome coronavirus (SARS-CoV) in the lungs of patients with SARS is important in confirming the etiol. assocn. of the virus with disease as well as in understanding the pathogenesis of the disease. To our knowledge, there have been no comprehensive studies investigating viral infection at the cellular level in humans. Methods and Findings: We collected the largest series of fatal cases of SARS with autopsy material to date by merging the pathol. material from two regions involved in the 2003 worldwide SARS outbreak in Hong Kong, China, and Toronto, Canada. We developed a monoclonal antibody against the SARS-CoV nucleoprotein and used it together with in situ hybridization (ISH) to analyze the autopsy lung tissues of 32 patients with SARS from Hong Kong and Toronto. We compared the results of these assays with the pulmonary pathologies and the clin. course of illness for each patient. SARS-CoV nucleoprotein and RNA were detected by immunohistochem. and ISH, resp., primarily in alveolar pneumocytes and, less frequently, in macrophages. Such localization was detected in four of the seven patients who died within two weeks of illness onset, and in none of the 25 patients who died later than two weeks after symptom onset. Conclusions: The pulmonary alveolar epithelium is the chief target of SARS-CoV, with macrophages infected subsequently. Viral replication appears to be limited to the first two weeks after symptom onset, with little evidence of continued widespread replication after this period. If antiviral therapy is considered for future treatment, it should be focused on this two-week period of acute clin. disease.
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 5 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN
Full Text | Cited References

ACCESSION NUMBER: 2005:562710 CAPLUS
DOCUMENT NUMBER: 143:246447
TITLE: Use of monoclonal antibodies in blocking ELISA

detection of transmissible gastroenteritis virus in faeces of piglets

AUTHOR(S): Rodak, L.; Smid, B.; Nevorankova, Z.; Valicek, L.; Smitalova, R.

CORPORATE SOURCE: Veterinary Research Institute, Brno, Czech Rep.

SOURCE: Journal of Veterinary Medicine, Series B (2005), 52(3), 105-111
CODEN: JVMBE9; ISSN: 0931-1793

PUBLISHER: Blackwell Verlag GmbH

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Monoclonal antibodies (mAb) to the transmissible gastroenteritis virus (TGEV) nucleoprotein (N) and membrane protein (M) were prepd. and used for the comparative assessment of three blocking ELISA variants to detect TGEV. The competitive blocking ELISA format showed the highest sensitivity, allowing detection of 103 TCID50 TGEV/mL in culture medium. Ninety-nine porcine field fecal samples obtained from 37 herds affected with diarrhea were examd., and various TGEV levels were found in nine samples from six herds. However, only in three samples were significant TGEV concns. demonstrated. The relationship between incidence of TGEV gastroenteritis and the spread of porcine respiratory coronavirus infection in pig farms is discussed.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2005:409560 CAPLUS

DOCUMENT NUMBER: 142:462283

TITLE: Monoclonal antibodies specific to SARS virus nucleoprotein for immunodiagnosis of SARS

INVENTOR(S): Uchida, Yoshiaki; Fujii, Nobuyuki; Kurano, Yoshihiro; Okada, Masahisa; Kogaki, Hiroyuki; Kido, Yasuji; Miyake, Kazushige

PATENT ASSIGNEE(S): Fujirebio Inc., Japan

SOURCE: PCT Int. Appl., 41 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: Japanese

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005042579	A1	20050512	WO 2004-JP16099	20041029
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CN 1902230	A	20070124	CN 2004-80039648	20041029
IN 2006KN01457	A	20070504	IN 2006-KN1457	20060530
US 20080254440	A1	20081016	US 2007-577310	20070222

PRIORITY APPLN. INFO.:	JP 2003-373779	A	20031031
	JP 2004-34268	A	20040210
	WO 2004-JP16099	W	20041029

AB Provided are monoclonal antibodies specific to SARS virus nucleoprotein and hybridomas producing them. These monoclonal antibodies are labeled with enzyme and used for immunodiagnosis of SARS.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Citing References

ACCESSION NUMBER: 2004:872877 CAPLUS
DOCUMENT NUMBER: 141:378847
TITLE: Endogenous host elements or viral-based sequence elements for diagnosis, prognosis and therapy of viral infection, autoimmune disease and lymphoproliferative disease
INVENTOR(S): Hu, Yu-wen; Brown, Earl
PATENT ASSIGNEE(S): Canadian Blood Services, Can.
SOURCE: PCT Int. Appl., 174 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004090544	A2	20041021	WO 2004-CA544	20040413
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2522067	A1	20041021	CA 2004-2522067	20040413
EP 1625402	A2	20060215	EP 2004-726942	20040413
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR				
US 20060115875	A1	20060601	US 2005-248008	20051011

PRIORITY APPLN. INFO.:	US 2003-461137P	P	20030409
	US 2003-506779P	P	20030930
	WO 2004-CA544	W	20040413

AB A method of detecting, characterizing and treating viral infection, autoimmune disease and lymphoproliferative disease is provided. In particular, a strategy of mol. mimicry is provided for characterizing viral behavior and/or a predisposition for a given viral outcome in vivo. Novel compns. are also provided for detecting, characterizing and treating viral infections. The viral infection is caused by HCV, HIV, HTLV-1, HTLV-2, SARS-CoV, or a member of Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae, Poxviridae or Coronaviridae. The viral-based sequence element is e.g. an element of S protein sequence of an ORF1a protein sequence of SARS-CoV; a Gag, Pol or Env polyprotein of HTLV-1; a NS5A and E2 protein of HCV; bacterial virulence factor; human

endogenous retrovirus element; Peyer's patches virulence factor gipA; or an Ig selected from IgG, IgA, IgM, IgD or IgE. The treatment regime includes an anti-viral monoclonal or polyclonal antibody, or a compd. capable of binding epitope of the endogenous host element.

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Full Text | More Reference

ACCESSION NUMBER: 2004:541777 CAPLUS
DOCUMENT NUMBER: 141:222968
TITLE: Organ distribution of severe acute respiratory syndrome (SARS) associated coronavirus (SARS-CoV) in SARS patients: implications for pathogenesis and virus transmission pathways
AUTHOR(S): Ding, Yanqing; He, Li; Zhang, Qingling; Huang, Zhongxi; Che, Xiaoyan; Hou, Jinlin; Wang, Huijun; Shen, Hong; Qiu, Liwen; Li, Zhuguo; Geng, Jian; Cai, Junjie; Han, Huixia; Li, Xin; Kang, Wei; Weng, Desheng; Liang, Ping; Jiang, Shibo
CORPORATE SOURCE: Department of Pathology, Nan Fang Hospital, First Military Medical University, Guangzhou, Peop. Rep. China
SOURCE: Journal of Pathology (2004), 203(2), 622-630
CODEN: JPTLAS; ISSN: 0022-3417
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We previously identified the major pathol. changes in the respiratory and immune systems of patients who died of severe acute respiratory syndrome (SARS) but gained little information on the organ distribution of SARS-assocd. coronavirus (SARS-CoV). In the present study, we used a murine monoclonal antibody specific for SARS-CoV nucleoprotein, and probes specific for a SARS-CoV RNA polymerase gene fragment, for immunohistochem. and in situ hybridization, resp., to detect SARS-CoV systematically in tissues from patients who died of SARS. SARS-CoV was found in lung, trachea/bronchus, stomach, small intestine, distal convoluted renal tubule, sweat gland, parathyroid, pituitary, pancreas, adrenal gland, liver and cerebrum, but was not detected in esophagus, spleen, lymph node, bone marrow, heart, aorta, cerebellum, thyroid, testis, ovary, uterus or muscle. These results suggest that, in addn. to the respiratory system, the gastrointestinal tract and other organs with detectable SARS-CoV may also be targets of SARS-CoV infection. The pathol. changes in these organs may be caused directly by the cytopathic effect mediated by local replication of the SARS-CoV; or indirectly as a result of systemic responses to respiratory failure or the harmful immune response induced by viral infection. In addn. to viral spread through a respiratory route, SARS-CoV in the intestinal tract, kidney and sweat glands may be excreted via feces, urine and sweat, thereby leading to virus transmission. This study provides important information for understanding the pathogenesis of SARS-CoV infection and sheds light on possible virus transmission pathways. This data will be useful for designing new strategies for prevention and treatment of SARS.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 9 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | More Reference

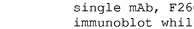
ACCESSION NUMBER: 2004:539287 CAPLUS
DOCUMENT NUMBER: 141:275951

TITLE: Development and characterisation of neutralising monoclonal antibody to the SARS-coronavirus
AUTHOR(S): Berry, Jody D.; Jones, Steven; Drebot, Michael A.; Andonov, Anton; Sabara, Marta; Yuan, Xin Y.; Weingartl, Hana; Fernando, Lisa; Marszal, Peter; Gren, Jason; Nicolas, Brigitte; Andonova, Maya; Ranada, Francesca; Gubbins, Michael J.; Ball, T. Blake; Kitching, Paul; Li, Yan; Kabani, Amin; Plummer, Frank
CORPORATE SOURCE: Department of Medical Microbiology, National Centre for Foreign Animal Disease, CFIA, University of Manitoba, Winnipeg, Can.
SOURCE: Journal of Virological Methods (2004), 120(1), 87-96 CODEN: JVMEDH; ISSN: 0166-0934
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB There is a global need to elucidate protective antigens expressed by the SARS-coronavirus (SARS-CoV). Monoclonal antibody reagents that recognize specific antigens on SARS-CoV are needed urgently. In this report, the development and immunochem. characterization of a panel of murine monoclonal antibodies (mAbs) against the SARS-CoV is presented, based upon their specificity, binding requirements, and biol. activity. Initial screening by ELISA, using highly purified virus as the coating antigen, resulted in the selection of 103 mAbs to the SARS virus. Subsequent screening steps reduced this panel to seventeen IgG mAbs. A single mAb, F26G15, is specific for the nucleoprotein as seen in Western immunoblot while five other mAbs react with the Spike protein. Two of these Spike-specific mAbs demonstrate the ability to neutralize SARS-CoV in vitro while another four Western immunoblot-neg. mAbs also neutralize the virus. The utility of these mAbs for diagnostic development is demonstrated. Antibody from convalescent SARS patients, but not normal human serum, is also shown to specifically compete off binding of mAbs to whole SARS-CoV. These studies highlight the importance of using standardized assays and reagents. These mAbs will be useful for the development of diagnostic tests, studies of SARS-CoV pathogenesis and vaccine development.

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN



ACCESSION NUMBER: 2001:48484 CAPLUS
DOCUMENT NUMBER: 134:219537
TITLE: The membrane M protein carboxy terminus binds to transmissible gastroenteritis coronavirus core and contributes to core stability
AUTHOR(S): Escors, David; Ortego, Javier; Laude, Hubert; Enjuanes, Luis
CORPORATE SOURCE: Department of Molecular and Cell Biology, Centro Nacional de Biotecnologia, CSIC, Madrid, 28049, Spain
SOURCE: Journal of Virology (2001), 75(3), 1312-1324 CODEN: JOVIAM; ISSN: 0022-538X
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The architecture of transmissible gastroenteritis coronavirus includes three different structural levels, the envelope, an internal core, and the nucleocapsid that is released when the core is disrupted. Starting from purified virions, core structures have been reproducibly isolated as

independent entities. The cores were stabilized at basic pH and by the presence of divalent cations, with Mg2+ ions more effectively contributing to core stability. Core structures showed high resistance to different concns. of detergents, reducing agents, and urea and low concns. of monovalent ions (<200 mM). Cores were composed of the nucleoprotein, RNA, and the C domain of the membrane (M) protein. At high salt concns. (200 to 300 mM), the M protein was no longer assocd. with the nucleocapsid, which resulted in destruction of the core structure. A specific ionic interaction between the M protein carboxy terminus and the nucleocapsid was demonstrated using three complementary approaches: (i) a binding assay performed between a collection of M protein amino acid substitution or deletion mutants and purified nucleocapsids that led to the identification of a 16-amino-acid (aa) domain (aa 237 to 252) as being responsible for binding the M protein to the nucleocapsid; (ii) the specific inhibition of this binding by monoclonal antibodies (MAbs) binding to a carboxy-terminal M protein domain close to the indicated peptide but not by MAbs specific for the M protein amino terminus; and (iii) a 26-residue peptide, including the predicted sequence (aa 237 to 252), which specifically inhibited the binding. Direct binding of the M protein to the nucleoprotein was predicted, since degrdn. of the exposed RNA by RNase treatment did not affect the binding. It is proposed that the M protein is embedded within the virus membrane and that the C region, exposed to the interior face of the virion in a population of these mols., interacts with the nucleocapsid to which it is anchored, forming the core. Only the C region of the M protein is part of the core.

REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | CBSA References

ACCESSION NUMBER: 1999:336041 CAPLUS
DOCUMENT NUMBER: 131:156705
TITLE: Production, characterization, and uses of monoclonal antibodies against recombinant nucleoprotein of elk coronavirus
AUTHOR(S): Daginakatte, Girish C.; Chard-Bergstrom, Cindy; Andrews, Gordon A.; Kapil, Sanjay
CORPORATE SOURCE: Department of Diagnostic Medicine-Pathobiology, College of Veterinary Medicine, Manhattan, KS, 66506, USA
SOURCE: Clinical and Diagnostic Laboratory Immunology (1999), 6(3), 341-344
CODEN: CDIMEN; ISSN: 1071-412X
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB This is the first report of the prodn. of monoclonal antibodies against elk coronavirus. The nucleoprotein gene of elk coronavirus was amplified by PCR and was cloned and expressed in a prokaryotic expression vector. Recombinant nucleocapsid protein was used to immunize mice for the prodn. of hybridomas. Twelve hybridomas that produced monoclonal antibodies against the nucleocapsid protein of elk coronavirus were selected by an indirect fluorescent-antibody test, an ELISA, and a Western blot assay. Ten of the monoclonal antibodies were of the IgG1 isotype, one was IgG2a, and one was IgM. All had kappa light chains. By immunohistochem. four monoclonal antibodies detected bovine coronavirus and elk coronavirus in formalin-fixed intestinal tissues. Anti-nucleoprotein monoclonal antibodies were better at ruminant coronavirus detection than the anti-spike protein monoclonal

antibodies. Because nucleoprotein is a more abundant antigen than spike protein in infected cells, this was not an unexpected finding.
REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN
Full Text String References
ACCESSION NUMBER: 1997:723088 CAPLUS
DOCUMENT NUMBER: 128:58017
ORIGINAL REFERENCE NO.: 128:11239a,11242a
TITLE: Isolation and characterization of a coronavirus from elk calves with diarrhea
AUTHOR(S): Majhdi, F.; Minocha, H. C.; Kapil, S.
CORPORATE SOURCE: Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS, 66506, USA
SOURCE: Journal of Clinical Microbiology (1997), 35(11), 2937-2942
CODEN: JCMIDW; ISSN: 0095-1137
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB This is the first report of the isolation of a coronavirus from elk calves. Two fecal samples from elk calves with diarrhea were shown to be pos. for coronavirus-like particles by electron microscopy, and the particles were propagated in the human rectal tumor-18 cell line. After 24 h, syncytia were obsd., and cell culture supernatants from both samples showed hemagglutinating activity with mouse erythrocytes. Cells infected with both elk coronavirus (ECV) isolates reacted with Z3A5, a monoclonal antibody against the spike protein of bovine coronavirus (BCV), on an indirect fluorescent antibody test. The protein profiles of both ECV isolates were similar to that of BCV as detd. by sodium dodecyl sulfate-polyacrylamide gel electrophoresis anal. On Northern blot anal., the transcriptional pattern of ECV was typical of coronaviruses, with a nested set of transcripts with common 3' end sequences. Based on a published nucleoprotein gene sequence for BCV (Mebus isolate), we arbitrarily designed two primers for amplification by PCR. After cloning, the nucleoprotein was sequenced and a high degree of homol. (99%) between the nucleoprotein gene sequences of ECV and BCV was obsd. Thus, ECV is closely related genetically and antigenically to BCV and will be a new member of antigenic group 2 of the mammalian coronaviruses, which possess hemagglutinin-esterase protein.

L15 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN
Full Text String References
ACCESSION NUMBER: 1991:533524 CAPLUS
DOCUMENT NUMBER: 115:133524
ORIGINAL REFERENCE NO.: 115:22845a,22848a
TITLE: Comparison of bovine coronavirus (BCV) antigens: monoclonal antibodies to the spike glycoprotein distinguish between vaccine and wild-type strains
AUTHOR(S): Hussain, Khalid A.; Storz, Johannes; Kousoulas, Konstantin G.
CORPORATE SOURCE: Sch. Vet. Med., Louisiana State Univ., Baton Rouge, LA, 70803, USA
SOURCE: Virology (1991), 183(1), 442-5
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal

LANGUAGE: English
AB Monoclonal antibodies (MAbs) against two major structural proteins of the cell-adapted Mebus strain of bovine coronavirus (BCV-L9) were produced and characterized. Seven MAbs reacted with the peplomeric glycoprotein, gp100/S, while three MAbs reacted with the nucleoprotein p53/N in Western blot anal. of BCV polypeptides. MAbs to gp100/S reacted with discontinuous epitopes of gp100/S in Westerns under mild but not under std. denaturing conditions. In contrast, MAbs to p53/N reacted in both types of Westerns, and those epitopes were thus continuous. MAbs to p53/N failed to neutralize BCV infectivity, while 4 MAbs to gp100/S neutralized BCV effectively. Cross reactivity of MAbs to gp100/S specified by five virulent wild-type strains and two high passage, cell-culture-adapted strains in mildly denaturing Westerns and neutralization assays indicated that two epitopes were conserved in all seven strains, while two epitopes of the avirulent strains were not detected in the wild-type strains. Non-neutralizing MAbs of gp100/S reacted with all seven strains in Westerns with the exception of one MAb that was specific for the highly cell-adapted strain BCV-L9.

L15 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Ring References

ACCESSION NUMBER: 1988:470029 CAPLUS
DOCUMENT NUMBER: 109:70029
ORIGINAL REFERENCE NO.: 109:11669a,11672a
TITLE: Antigenic differentiation between transmissible gastroenteritis virus of swine and a related porcine respiratory coronavirus
AUTHOR(S): Callebaut, P.; Correa, I.; Pensaert, M.; Jimenez, G.; Enjuanes, L.
CORPORATE SOURCE: Fac. Vet. Med., State Univ. Gent, Ghent, B-9000, Belg.
SOURCE: Journal of General Virology (1988), 69(7), 1725-30
CODEN: JGVIAY; ISSN: 0022-1317
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The antigenic relationship between isolated porcine respiratory coronavirus (TLM 83) and transmissible gastroenteritis (TGE) virus of swine was studied by neutralization, immunoblotting, and RIA, using TGE virus-specific monoclonal antibodies (MAbs) and polyclonal antibodies specific for both viruses. A complete two-way neutralization activity between the two viruses was found. Immunoblotting revealed cross-reactions between TLM 83 and TGE virus antigens at the level of the envelope protein (E1), the nucleoprotein (N), and the peplomer protein (E2). By virus neutralization assays and RIA with TGE virus-specific MAbs, the presence of similar epitopes in the E1 and N proteins and in the neutralization-mediating antigenic site of the E2 protein were demonstrated. E2 protein-specific MAbs, without neutralizing activity and reacting with antigenic sites B, C, and D (previously defined), failed to recognize TLM 83. These results indicated a close antigenic relationship and structural similarity between TLM 83 and TGE viruses and also suggested potential ways of differentiating between the two viruses.

L15 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2009 ACS on STN

Full Text | Ring References

ACCESSION NUMBER: 1984:3195 CAPLUS
DOCUMENT NUMBER: 100:3195
ORIGINAL REFERENCE NO.: 100:551a,554a
TITLE: Synthesis and subcellular localization of the murine coronavirus nucleocapsid protein

AUTHOR(S): Stohlman, Stephen A.; Fleming, John O.; Patton, Chris D.; Lai, Michael M. C.
CORPORATE SOURCE: Sch. Med., Univ. South. California, Los Angeles, CA, 90033, USA
SOURCE: Virology (1983), 130(2), 527-32
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The synthesis and processing of the nucleocapsid protein (pp60) of the JHM strain of murine coronaviruses were examd. Pulse-chase expts. showed that pp60 was synthesized initially as a protein of mol. wt. ~57,000 (p57). Immunopptn. using mouse anti-JHMV antiserum indicated that p57 was virus specific. Immunopptn. with monoclonal antibodies specific for pp60 showed that p57 was antigenically related to pp60 and was not phosphorylated, whereas the intracellular protein that comigrated with the virion nucleocapsid protein, pp60, was phosphorylated. The p57 was found exclusively in the cytosol whereas the majority of pp60 was assocd. with the membrane fraction but pp60 was not an integral membrane protein.

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